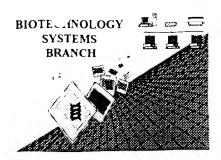
0590

# RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:	09/911,826
Source:	OlPE
Date Processed by STIC:	8/7/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: <a href="mailto:patin21help@uspto.gov">patin21help@uspto.gov</a> or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: <a href="mailto:patin3help@uspto.gov">patin3help@uspto.gov</a> or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

## **Checker Version 3.0**

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker

# Raw Sequence Listing Error Summary

RROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 09/91/826
TTN: NEW RULES CASE	S: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SO
1Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5Variable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6PatentIn 2.0 "bug"	A "bug" in Patentin version 2.0 has equence fire <220>-<223> section to be missing from amino acid sequences(s)
7Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:  (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  This sequence is intentionally skipped
, ,	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8Skipped Sequences (NEW RULES)	Sequence(s) missing. If Intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing.  Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
Use of <220>	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.  Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
Patentin 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001

OIPE

## TATE: : :: 01 RAW SEQUENCE LISTING PATENT APPLICATION: US/09/911,826 FIME: 13:57:06 Imput Set : A:\sequence-as filed.txt Output Set: N:\CRF3\08072001\I911826.raw 3 <110 - APPLICANT: HSC Research Development limited Partnership et a. $\gamma$ <120 $\cdot$ TITLE OF INVENTION: RAS Activator Nucleic Acid Molecules, Polypeptides and Methods of Use ∃ <130 · FILE REFERENCE: 1786/0019 $C_{\Gamma}$ > 10 <140> CURRENT APPLICATION NUMBER: US/09/911,826 €+-> 11 <141> CURRENT FILING DATE: 2001-07-20 13 <150 PRIOR APPLICATION NUMBER: 2,259,830 14 <151 PRIOR FILING DATE: 1999-01-20 16 K160% NUMBER OF SEQ ID NOS: 27 15 <1700 SOFTWARE: PatentIn Ver. 2.1 Does Not Comply ERRORED SEQUENCES Corrected Diskette Needed 6+6 -2105 SEQ IE NO: 4 697 HARLE LENGTH: 286 698 -3212 - TYFE: PRT 649 (213) CRGANISM: Homo sapiens 701 -400, SEQUENCE: 4 702 Thr Lys Gly Asr. Lys Ser Trp Ser Ser Thr Ala Val Ala Ala Ala Leu 70:3 705 Glu Leu Val Asp Pro Pro Gly Cys Arg Asn Ser Ser Gly Gly Lys Asp 706 70% Val Ser Ala Glu Ala Glu Ser Ser Ser Met Val Pro Val Thr Thr Glu 709 40 711 Glu Ala Lys Pro Val Pro Met Pro Ala His Ile Ala Val Thr Pro Ser 712 50 55 714 Thr Thr Lys Gly Led Ile Ala Ard Lys Glu Gly Ard Tyr Ard Glu Pro 715 65 717 Pro Pro Thr Pro Pro Gly Tyr Val Gly lle Fro Ile Ala Asp Phe Fro 718 7.0 Glu Gly Pro Cya His Pro Ala Arg Lys Pro Pro Asp Tyr Ash Val Ala 7.1 7.3 Leu Glm Arg Ser Ary Met Mal Ala Arg Fro Thr Elu Ala Fro Ala Fro 115 700 Gly Glr. Thr Pro Pro Ala Ala Ala Ala der Arm Pro Gly der Lys Pro 130 135 7.9 3ln Trp His Lys Pro Ser Asp Ala Asp Hib Ard Leu Ala Pro Phe Glu 7 10 145 161 791 Ala Ala Ser His Ser Aly Thr Ser Fro Ala Thr Alh Thr His Ala Ser 700 Arg Pro Ser Arg Sin Ala Ser Win Wid Arg Arg Arg Thr Lys Met Ash

E--> 738 Lys Cys Leu Leu Phe Glu Ala Gln Ala Pro/Xaa Ser Thr Val Ser His

[41 Fro Lys 31d Not The Ard Ary Ard Er. 198 Er. Top New Yes Sty Tha

Ever 9 in Ever Juman Heet 87

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#### RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/911,826

DATE: Washaring 01 TIME: 13:57:16

intut Jet : A:\sequence-as filed.txt Curput Set: N:\CRF3\08072001\I911826.raw

E--> 744 His Ile Xaa Gly Trp Trp Thr Ser Leu Pro Pro Ser Leu Pro Xaa Ser 745 325 230 .. ; 5 1.40

747 Ser Met Gly Leu Leu Leu Pro Phe Phe Leu Wer Fro Leu His Val Lys

748 245 ٠ ـ ـ ـ ـ ـ ـ

E--> 750 Tyr Cys Glu Glu Ile Ala Leu Ala Leu Cys Arg Leu Val Ala Xaa Asn 751 200 2.65

E--> 753 Ala Gln Pro Ser Ser Pro Xaa Ala Ala Ala Cys His Val Thr 280

754 275

7%7 <110 > SEQ ID NO: 5

7-3 -311: LENGTH: 245 759 CL120 TYPE: PRT

700 -0113: DRGANISM: Homo sapiens

761 -: 400> SEQUENCE: 5

E--> 763 Leu Lys Gly Thr Lys Ala Gly Ala Pro Pro Arg Trp Arg Pro Leu Xaa

E--> 766 Asn Xaa Trp Ile Pro Arg Ala Ala Gly Ile Gln Ala Val Gly Arg Met 25 20

E--> 769 Ser Pro Leu Arg Gln Arg Ala Ala Ala Trp Cys Pro Xaa Leu Gln Arg 770 3,5 4.0

E--> 772 Lys Pro Asn Leu Ser Leu Cys Leu Pro Thr Xaa Leu Xaa Arg Arg Ala

773 50 55 775 Leu Pro Arg Asp Ser Ser His Gly Arg Lys Ala Gly Thr Gly Ser Arg 774 65 7.0

77% Leu Pro His Leu Glm Ala Thr Trp Ala Ser Pro Leu Pro Ile Ser Glm 774 8.5 90

781 Lys Gly Leu Ala Thr Arg Pro Gly Ser Fro Arg Ile Thr Thr Trp Pro 731 100 105 110

784 Cys Ser Gly Pro Ala Trp Trp His Gly Pro Leu Arg Pro Arg His Arg 1.15

787 Ala Arg Arg Leu Gln Pro Gln Pro Ala Gly Arg Arg Leu Arg Arg 758 130 135 140

E--> 790 Ser Gly Gly Gly Arg Arg Xaa Thr Ser Val Cys Cys Leu Arg Arg Arg 7 (1 145 1,50 155 -160

E--> 793 Leu Leu Asp Pro Gln Xaa Ala Thr Gln Arg Arg Ala Gln Glu Asp Val 165

796 Pro Ser Leu Gly Ala Neu Ala Arg Thr Ser Glu Asp Gly Gly Pro Val 180 185

744 Cys Leu Leu Pro Cys Léu Lys Ala Ala Trp Fly Fhe Phe Ser Fro Ser

E--> 802 Ser Phe Pro Leu Cys Met Xaa Asn Thr Val Lys Lys Leu Pro Trp His XIII 9 8 .: 213 215

835 Phe Ala Asp Leu Leu Glu Met His Ser Pro Ala Ala Pro Glu Leu

80% Leu Pro Ala Thr Ser

80+

812 - L10 - SEQ ID Nº: 6

813 <211 - LENGTH: 1066 814 <212 > TYPE: PRT

815 - 213 - GRG/MICM: Home say tens

### RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/911,826

LATE: 0.8/10/72211 TIME: 13:57:16

Imput Set : A:\sequence-as filed.txt
Output Set: N:\CRF3\08072001\I911826.raw

			)> SI															
E>	<b>818</b>		Arg	Glu	Gln	Lys	Leu	Glu	Leu	His	Arg	Gly	Gly	Gly	Arg	Ser	Arg	1.0.06
			Ser	Gly	Sor	lro	Siy	Leu	Jir.	111	11	Lys	Arg	Tr	Glu	3) <u>1</u>	rys	-X0.11
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		Ser	Glr.	400 10 7	in ea	Fro	Ter	ā:a	Cus	Lynn	H 5 &	de et	'es	Asr.	Ai.a	11.11	His	
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		Arg	Ala	Leu	Pro	Pro	Gly	Gln	Glu	Ala	Fro	Gly	Leu	Gln	Arg	Gly	Pro	Ġ
	337				100					105					110			Jim
E>	839 940	Ala	Ala	<b>Val</b> 115	Pro	His	Gly		<b>Thr</b> 120	Ala	His	Xaa	Gly	Pro	Gly	Thr	Gly	$\mathcal{N}^{\cup}$
		Pro	Asp		Ala	Cvs	Ser			Gin	Pro	Ala	Ğlv		Gln	Ala	Thr	
	343		130			1 -		135					140					
			Alà	Gln	Ala	Glr.		Arg	Arg	Fro	Thr		Arg	Ala	Leu	Pro		
		145	Gly	Dha	7 1 m	~1	150	<i>~</i> 233	, - 1	7 an	23	155	~ , ,	/7.1 m	Wal	C	160	- <sub>C4</sub>
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E>		Val	Xaa	Gly	Ala		Ser	Leu	Ile	His	Ser	Glu	Pro	Pro	Lys	Gly	Glu	~~~
	852			_	180					185					190			,
	854 855	His	Lys	Lys 195	Thr	Ser	Gln	Ala	Leu 200	Glu	Pro	Trp	His	Ala 205	His	Leu	Arg	_
		M+>+	Vāl		Gln	Phe	Ala	Ser		Pro	Ala	Leu	Lvs		His	Glv	Ala	G
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E>			Ser	Pro	Leu	Leu		Phe	Pro	Phe	Ala		Glu	Ile	Leu	Xaa		
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		Gln	Pro	Leu	Ser		Cys	Leu	Fro	Arg	His							
	857				260					165								

#### VERIFICATION SUMMARY

PATENT APPLICATION: US/09/911,826

DATE: 08/07/2001 TIME: 13:57:07

Input Set : A:\sequence-as filed.txt
Output Set: N:\CRF3\08072001\1911826.raw

- L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
- L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
- L:406 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
- L:738 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4
- M:340 Repeated in SeqNo=4
- L:763 M:340 E: (46) "r." or "Xaa" used: Feature required, for SEQ ID#:5
- M:340 Repeated in SeqNo=5
- L:818 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
- M:340 Repeated in SeqNo=6
- L:1335 M:258 W: Mandatory Feature missing,  $\sim$ 221  $\sim$  not found for SEQ ID#:15
- L:1235 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:15
- L:1235 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15